*somniferum* cell suspension cultures. Peptide 1 is SEQ ID NO: 1, Peptide 2 is SEQ ID NO: 2, Peptide 2' is SEQ ID NO: 3, Peptide 3 is SEQ ID NO: 4, Peptide 3' is SEQ ID NO: 5, Peptide 4 is SEQ ID NO: 6, Peptide 5 is SEQ ID NO: 7, Peptide 6 is SEQ ID NO: 8, and Peptide 7 is SEQ ID NO: 9.--

B1 cont'd

Please replace the paragraph beginning at page 9, line 9, with the following rewritten paragraph:

--**Figure 3.** Partial amino acid sequence comparison of plant cytochrome P-450 reductases. The shaded areas and arrows indicate the position and direction of the regions used for PCR oligodeoxynucleotide primer design. Arabidopsis thaliana is SEQ ID NO: 20, Catharanthus roseus is SEQ ID NO: 21, Helianthus tuberosus is SEQ ID NO: 22, Vigna radiata is SEQ ID NO: 23 and Vicia sativa is SEQ ID NO: 24.--

B2

Please replace the paragraph beginning at page 9, line 18, with the following rewritten paragraph:

--**Figure 5.** Comparison of the amino acid sequences of the cytochrome P-450 reductase from *P. somniferum* and from *E. californica*. Top sequence, *E. californica*, SEQ ID NO: 25; bottom sequence, *P. somniferum*, SEQ ID NO: 26; *, amino acid identity.--

B3

Please replace the paragraph beginning at page 9, line 21, with the following rewritten paragraph:

--**Figure. 6.** Nucleotide sequences of cDNA from (a) *P. somniferum*, SEQ ID NO: 10 and (b) *E. californica*, SEQ ID NO: 11.--

B4

Please replace the paragraph beginning at page 9, line 32, with the following rewritten paragraph:

B5

--**Figure 9.** Amino acid sequences of (a) *P. somniferum*, SEQ ID NO: 12 and SEQ ID NO: 13 and (b) *E. californica*, SEQ ID NO: 14 and SEQ ID NO: 15 predicted from their respective cDNA nucleotide sequences. The start and stop codons are depicted in bold.--

Please replace the paragraph beginning at page 10, line 1, with the following rewritten paragraph:

B4

--**Figure 10.** cDNA nucleotide sequences and their predicted amino acid sequences, of fragments subcloned into an expression vector: (a) *P. somniferum*, SEQ ID NO: 16 and SEQ ID NO: 17 and (b) *E. californica*. Both sequences are truncated versions of sequences represented in Figures 9a and 9b, lacking the leader sequences. Extra vector sequences/restriction sites derived during subcloning are shown in lowercase and the cDNA in uppercase.--

Please replace the paragraph beginning at page 16, line 11, with the following rewritten paragraph:

B7

-- Optimised PCR primers were then designed based on highly homologous sites on both the amino acid and nucleotide levels in the plant cytochrome P-450 reductase sequence comparison (Fig. 3). The precise sequence of the primers used for the first round of PCR was:

5'-CA ITI CII CCT CCT TTC CC-3' SEQ ID NO: 27 and
T SEQ ID NO: 28

B1 cont'd

3'-ACC TAC TTC TTA CGI CAA GG-5'. SEQ ID NO: 29
C TGC SEQ ID NO: 30

Please replace the paragraph beginning at page 17, line 4, with the following rewritten paragraph:

Resolution of this first PCR experiment by agarose gel electrophoresis revealed a mixture of DNA products in the expected range of 400-450 bp. The bands in this size range were eluted from the gel and used as template for nested PCR with the following primers:

B8

5'-CA ITI CII CCT CCT TTC CC-3' SEQ ID NO: 27 and
T SEQ ID NO: 28

3'-AAA CGI CGI TAI CGI GGI GCI IGI GTT GG-5' SEQ ID NO: 31
G C SEQ ID NO: 32